

Figure 1A

1	ATGACAACTCTGTTCTGCAACCCTCTCCCTCTCTCTGGACCCGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTTCTAGACAAACTATGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTGGCCCAATTAAAGGCCACCGTGAAACGTGACCTGCAACATCTTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTGCGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTGGACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGAAATGTG	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCCCTCATTTGTCCTGCCTGATGGACCTCAAGAACTTCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTGGCTACACCATGAAAGACCTC	600
181	M D I Q T C T M Q L E S <u>F G Y</u> T M K D L	200
601	GTGTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGCTGACTCTGCC	660
201	V F E W L E D A P A V Q V A E G L T L P	220
661	CAGTTTATCTGCGGGATGAGAAGGATCTAGGCTGTTGACCAAGCACTACAACACAGGG	720
221	Q F I L R D E K D L G C C T <u>K H Y N T</u> G	240
721	AAATTCACCTGCATCGAGGTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATT	780
241	K F T C I E V K F H L E R Q <u>M G Y Y L I</u>	260
781	CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTCTGGATCAAC	840
261	<u>Q M Y I P S L L I V I L S W V S F W I N</u>	280
841	ATGGATGCTGCCCTGCCCCTGGGCTGGGCATCACCAACCGTGCTCACCATGACCACC	900
281	<u>M D A A P A R V G L G I T T V L T M T T</u>	300

Figure 1B

901	CAGAGCTCTGGCTCCGGGCCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATC	960
301	<u>Q S S G S</u> R A S L P K V S Y V K A I D <u>I</u>	320
961	TGGATGGCTGTGTCTGCTCTTGTGTTGCTGCCTGCTGGAGTATGCTGCCATAAAT	1020
321	<u>W M A V C L L F V F A A L L E Y A A I N</u>	340
1021	TTTGTTCCTCGTCAGCATAAAGAATTACGACTTCGAAGAAGGCAGAGGCGCCAACGC	1080
341	<u>F V S</u> R Q H K E F I R L R R R Q R R Q R	360
1081	TTGGAGGAAGATATCATCCAAGAAAGTCGTTCTATTCCGTGGCTATGGCTGGCCAC	1140
361	L E E D I I Q E S R F Y F R G Y G L G H	380
1141	TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCT	1200
381	C L Q A R D G G P M E G S G I Y S P Q P	400
1201	CCAGCCCCCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAG	1260
401	P A P L L R E G E T T R K L Y V D	417
1261	AGAATTGACACCATCTCCGGCTGTCTCCCTTCACTTCCCTCATCTCAATATCTTC	1320
1321	TACTGGTTGTCTATAAGTGCACGGTCAGAAGATATCCACCCAGGCTGTGAATAGGG	1380
1381	TGGGAGCTATAGAGTCCTGCTGCTGGCCTCCTGCTTCCTGGTGGCTTCTCCCTC	1440
1441	AGTTAGACTCCATTAGGGTTGGACAGTTCCCTGATCTCCACTCAGAACTCAAC	1500
1501	TACCAAGTCCAAAGCTATGTGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATA	1560
1561	AAGATGGCTTATCTACCCCTAGTCATATTTCTCCATACTTCCCATTCTCATGAGACT	1620
1621	AAGGTTGGCCACATTCCCTGGGCCAGGATGACCTCTGCCCTGCTGGAGCCTCCGT	1680
1681	TTTCCAATACTCCAGTGGAGAGTATTCAAGAACACTGCTGCTAGATTCTGGCATTGTCAT	1740
1741	CTTAATCTGCACCACTTCTCCCCCTGCCACCTCCCACCCAGAGCCTGGCCATTACTCTGT	1800
1801	CCTCTGTCCCTCTGCTGCAGATTCAAATGGTGAGTTCTCCTATCCACAAAGTGCTGCC	1860
1861	TGTGGGGCCTAGTCAGGTTCTTGAAGTGAGAGGAAGGCAAAGCCGCAAGTCCCCACC	1920
1921	TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGCTAGCGACTATATGGCCCAACAG	1980

Figure 1C

1981 AGAGGTGTTCAAGTCTCTGGGAAGCCCCACACTTGTCTTCATCCCTTCCTATTGCG 2040
2041 CTTGTCTGCTCTTCCTGTTCACTGAGATACTCCTCTGTCTGTCTCTAGTTGAGGA 2100
2101 GAGCGTTCTGAGCTGACCAGGGTAGCTGGTCAGAAATTACTGTCAGAATTGGGGCAGAG 2160
2161 ACTTTGGGTTCTCAAAAAGACTAACCTCCAGATCCACCTGAACATTCTGGTCTCAGAAA 2220
2221 TATTGTTCCCGTCCCTAATTAACCTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGAG 2280
2281 TGTAAAAAAAGAAAAACTTGTCTTTAAGAAACTTACTTATGATGCTAGAAAACCTT 2340
2341 TGAGAAAAGTGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAGAATAGAGAAACTATTCT 2400
2401 CAGAGTGTCTTGTGGCTGGCTTCATTTGTTCTTCTCACCAAAGTCTATT 2460
2461 TCCAGGGCCCTCATTCCAACCTGGTCTTCACCTCCTTGGTGTGCAAATAAGGTG 2520
2521 CCGCTGCAACCTGTTAAGGATAAAAAAAAAAAAAAAA 2565

Figure 2A

1 ATGACAACTCTGTTCTGCAACCCCTCCCTCCTCTCTGGACCCGCCAGGGCAG 60
 1 M T T L V P A T L S F L L L W T L P G Q 20

61 GTCCTCCTCAGGGTGGCCTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCAG 120
 21 V L L R V A L A K E E V K S G T K G S Q 40

121 CCCATGTCCCCCTCTGATTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC 180
 41 P M S P S D F L D K L M G R T S G Y D A 60

181 AGGATTCGGCCAATTTAAAGGCCACCGTGAAACGTGACCTGCAACATCTCATCAAC 240
 61 R I R P N F K G P P V N V T C N I F I N 80

241 AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTGCGGCAA 300
 81 S F S S V T K T T M D Y R V N V F L R Q 100

301 CAGTGGAAATGACCCACGCCTGCTTACCGAGAAATATCCTGATGACTCTGGACCTCGAT 360
 101 Q W N D P R L S Y R E Y P D D S L D L D 120

361 CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGCC 420
 121 P S M L D S I W K P D L F F A N E K G A 140

421 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGAAATGTG 480
 141 N F H E V T T D N K L L R I F K N G N V 160

481 CTGTACAGCATCAGGCTGACCCCTCATTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC 540
 161 L Y S I R L T L I L S C L M D L K N F P 180

541 ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG 600
 181 M D I Q T C T M Q L E S S S I L C S P L 200

601 CCATCTCTGTCACTTCAAGTTGGCTACACCATGAAAGACCTCGTGTGAGTGGCTGGAA 660
 201 P S L S L S V **S** T M K D L V F E W L E 220

661 GATGCTCCTGCTGTCCAAGTGGCTGAGGGCTGACTCTGCCCTGAGTTATCTGGGGAT 720
 221 D A P A V Q V A E G L T L P Q F I L R D 240

721 GAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTACACCTGCATCGAG 780
 241 E K D L G C C T **K** **K** **X** **X** G K F T C I E 260

781 GTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATTGAGATGTACATCCCCAGC 840
 261 V K F H L E R Q M G Y Y L I Q M Y I P S 280

841 CTACTCATCGTCATCCTGTCCTGGCTCCTCTGGATCAACATGGATGCTGCCCTGCC 900
 281 L L I V I L S W V S F W I N M D A A P A 300

Figure 2B

901	CGTGTGGGCCTGGGCATCACCAACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCGG	960
301	R <u>V</u> <u>G</u> <u>L</u> <u>G</u> <u>I</u> <u>T</u> <u>T</u> <u>V</u> <u>L</u> <u>T</u> <u>M</u> <u>T</u> <u>T</u> <u>Q</u> <u>S</u> <u>S</u> <u>G</u> <u>S</u> <u>R</u>	320
961	GCCTCTTGCCTAAGGTGTCCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTCTG	1020
321	A <u>S</u> <u>L</u> <u>P</u> <u>K</u> <u>V</u> <u>S</u> <u>Y</u> <u>V</u> <u>K</u> <u>A</u> <u>I</u> <u>D</u> <u>I</u> <u>W</u> <u>M</u> <u>A</u> <u>V</u> <u>C</u> <u>L</u>	340
1021	CTCTTGTTGTCGCTGCCCTGGAGTATGCTGCCATAAATTGTTCTCGTCAGCAT	1080
341	<u>L</u> <u>F</u> <u>V</u> <u>F</u> <u>A</u> <u>A</u> <u>L</u> <u>L</u> <u>E</u> <u>Y</u> <u>A</u> <u>A</u> <u>I</u> <u>N</u> <u>F</u> <u>V</u> <u>S</u> <u>R</u> <u>Q</u> <u>H</u>	360
1081	AAAGAATTCAACGACTTCGAAGAAGGCAGAGGCAGGCCAACGCTTGGAGGAAGATATCATC	1140
361	K <u>E</u> <u>F</u> <u>I</u> <u>R</u> <u>L</u> <u>R</u> <u>R</u> <u>Q</u> <u>R</u> <u>R</u> <u>Q</u> <u>R</u> <u>L</u> <u>E</u> <u>E</u> <u>D</u> <u>I</u> <u>I</u>	380
1141	CAAGAAAGTCGTTCTATTCCGTGGCTATGGCTTGGCCACTGCCTGCAGGAAGAGAT	1200
381	Q <u>E</u> <u>S</u> <u>R</u> <u>F</u> <u>Y</u> <u>F</u> <u>R</u> <u>G</u> <u>Y</u> <u>G</u> <u>L</u> <u>G</u> <u>H</u> <u>C</u> <u>L</u> <u>Q</u> <u>A</u> <u>R</u> <u>D</u>	400
1201	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCCCTTTCTAAGG	1260
401	<u>G</u> <u>G</u> <u>P</u> <u>M</u> <u>E</u> <u>G</u> <u>S</u> <u>G</u> <u>I</u> <u>Y</u> <u>S</u> <u>P</u> <u>Q</u> <u>P</u> <u>P</u> <u>A</u> <u>P</u> <u>L</u> <u>L</u> <u>R</u>	420
1261	GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC	1320
421	E <u>G</u> <u>E</u> <u>T</u> <u>T</u> <u>R</u> <u>K</u> <u>L</u> <u>Y</u> <u>V</u> <u>D</u>	431
1321	CGGGCTGTCTCCCTTCACTTCCTCATCTCAATATCTTCTACTGGGTTGTCTATAAA	1380
1381	GTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGAGCTATAGAGTCCT	1440
1441	GCTGCTGGCCTCCTGCTCCTGGTGGCTTCTCCCTCAGTTAGACTCCATTAGGG	1500
1501	GTGGACAGTTCCCTGATCTCCACTCAGAACTCAACTACCAGTCCAAAGCTAT	1560
1561	GTGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC	1620
1621	TAAAAAAAAAAAAAAAAAAA 1640	

Figure 3A

1 -----MYSFNTLRLYLSGAIVFSLAASKAEEAARSATKPMSPSDFLDK
 GRA3_HUMAN (1) -MAHVRHFRTLVSGFYWEAALLSLVATKEFDSARSRSAPMSPSDFLDK
 HGRA4 (1) MTLVLPATLSFLLLWTLPGQVLLRVALAKEEVKSGKKGQPMSPSDFLDK
 HGRA4_sv (1) MTLVLPATLSFLLLWTLPGQVLLRVALAKEEVKSGKKGQPMSPSDFLDK
 GRA4_MOUSE (1) -----VALAKEDVKSLKGQPMSPSDFLDK
 GRA2_HUMAN (1) MNRQIVNILTALEAFFLETNHFRTAFCKDHDSSRGKOPSQTLSPSDFLDK

51 100
 GRA1_HUMAN (45) LMGRSGYDARIRPNFKGPPVNVSCNIFINSFGSIAETTMDYRVNITFLRQ
 GRA3_HUMAN (50) LMGRSGYDARIRPNFKGPPVNVTCNIFINSFGSIAETTMDYRVNITFLRQ
 HGRA4 (51) LMGRSGYDARIRPNFKGPPVNVTCNIFINSFGSIVTTMDYRVNITFLRQ
 HGRA4_sv (51) LMGRSGYDARIRPNFKGPPVNVTCNIFINSFGSIVTTMDYRVNITFLRQ
 GRA4_MOUSE (27) LMGRSGYDARIRPNFKGPPVNVTCNIFINSFGSIVTTMDYRVNITFLRQ
 GRA2_HUMAN (51) LMGRSGYDARIRPNFKGPPVNVTCNIFINSFGSIVTTMDYRVNITFLRQ

101 150
 GRA1_HUMAN (95) QWNPDPRLAYNEYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK
 GRA3_HUMAN (100) KWNPDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK
 HGRA4 (101) QWNPDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK
 HGRA4_sv (101) QWNPDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK
 GRA4_MOUSE (77) QWNPDPRLAYREYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK
 GRA2_HUMAN (101) QWNPDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFFANEKGAFHETITTDNK

151 200
 GRA1_HUMAN (145) LLRISRNGNVLYSIRTLTLACPMMDLKNFPMDVQTCIMQLES-----
 GRA3_HUMAN (150) LLRIFKNGNVLVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----
 HGRA4 (151) LLRIFKNGNVLVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----
 HGRA4_sv (151) LLRIFKNGNVLVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----
 GRA4_MOUSE (127) LLRIFKNGNVLVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----
 GRA2_HUMAN (151) LLRISKNGKVLVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----

201 250
 GRA1_HUMAN (187) -----FGYTMNDLIFEWQEOGA-VQVADGLTLPQFILKEEKDLRYCTKH
 GRA3_HUMAN (192) -----FGYTMNDLIFEWQDEAP-VQVAEGLTLPQFILKEEKDLRYCTKH
 HGRA4 (193) -----FGYTMNDLIFEWQLEDAPA-VQVAEGLTLPQFILRDEKDGLGCTKH
 HGRA4_sv (201) PSLSLSVGYTMNDLIFEWQLEDAPA-VQVAEGLTLPQFILRDEKDGLGCTKH
 GRA4_MOUSE (169) -----FGYTMNDLIFEWQLEDAPA-VQVAEGLTLPQFILRDEKDGLGCTKH
 GRA2_HUMAN (193) -----FGYTMNDLIFEWLSDG-P-VQVAEGLTLPQFILKEEKELGYCTKH

251 [<<<<<<<<<TM1>>>>>>>>>] 300
 GRA1_HUMAN (230) YNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA
 GRA3_HUMAN (235) YNTGKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA
 HGRA4 (237) YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA
 HGRA4_sv (251) YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA
 GRA4_MOUSE (213) YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA
 GRA2_HUMAN (236) YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVTSFWINMDAAPA

3 [<<<<<<<<<TM2>>>>>>] [<<<<<<<<<TM3>>>>>>>>>]
 GRA1_HUMAN (280) RVLGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFSALLEY
 GRA3_HUMAN (285) RVALGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFSALLEY
 HGRA4 (287) RVLGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY
 HGRA4_sv (301) RVLGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY
 GRA4_MOUSE (263) RVLGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY
 GRA2_HUMAN (286) RVALGLGITTVLTMTTQSNSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY

Figure 3B

		>>>>>]			
GRA1_HUMAN	(330)	AAVNFVSRQHKELLRERRKRR-----		HHKEDEAGEGRFNFS	400
GRA3_HUMAN	(335)	AAVNFVSRQHKELLRERRKRKKNKTEAFALEKFYRFSMDDEVRESRFSF			
HGRA4	(337)	AAIINFVSRQHKEFIRLRRRQR-----		RQRNEEDIHOESRFYFR	
HGRA4sv	(351)	AAIINFVSRQHKEFIRLRRRQR-----		RQRNEEDIHOESRFYFR	
GRA4_MOUSE	(313)	AAVNFVSRQXKEFMRLLRRRQR-----		RQRM	
GRA2_HUMAN	(336)	AAVNFVSRQHKEFIRLRRRQR-----		RQNEEDVIRESRFNFS	
		401			450
GRA1_HUMAN	(366)	AYGMGPACLQAKDGISVKGANNSTTNPPPAPSKSPEEMRKLFIDRAKKI			
GRA3_HUMAN	(385)	AYGMGP-CLQAKDGMPKGP-----HPVQVMPKSPDEMRKVFDIDRAKKI			
HGRA4	(375)	GYGMGH-CLOAQARDGGPMEGS-GIYSPQPPAPILLREGETTRKLIVD-----			
HGRA4sv	(389)	GYGMGH-CLOAQARDGGPMEGS-GIYSPQPPAPILLREGETTRKLIVD-----			
GRA4_MOUSE	(338)	-----			
GRA2_HUMAN	(374)	GYGMGH-CLQVKDGTAVKATPANPLPQPPK-----DGDATKKKFVDRAKRI			
		451			487
GRA1_HUMAN	(416)	DKISRIGFPMAFLIFNMFYWLIYKIVRREDVHNO-----			
GRA3_HUMAN	(429)	DTISRACFPMAFLIFNMFYWVIYKIVRHEDVHHQQD			
HGRA4	(418)	-----			
HGRA4sv	(432)	-----			
GRA4_MOUSE	(338)	-----			
GRA2_HUMAN	(419)	DTISRAAFPMMAFLIFNMFYWLIYKIVRHEDVHKK-----			

卷之三

Figure 4

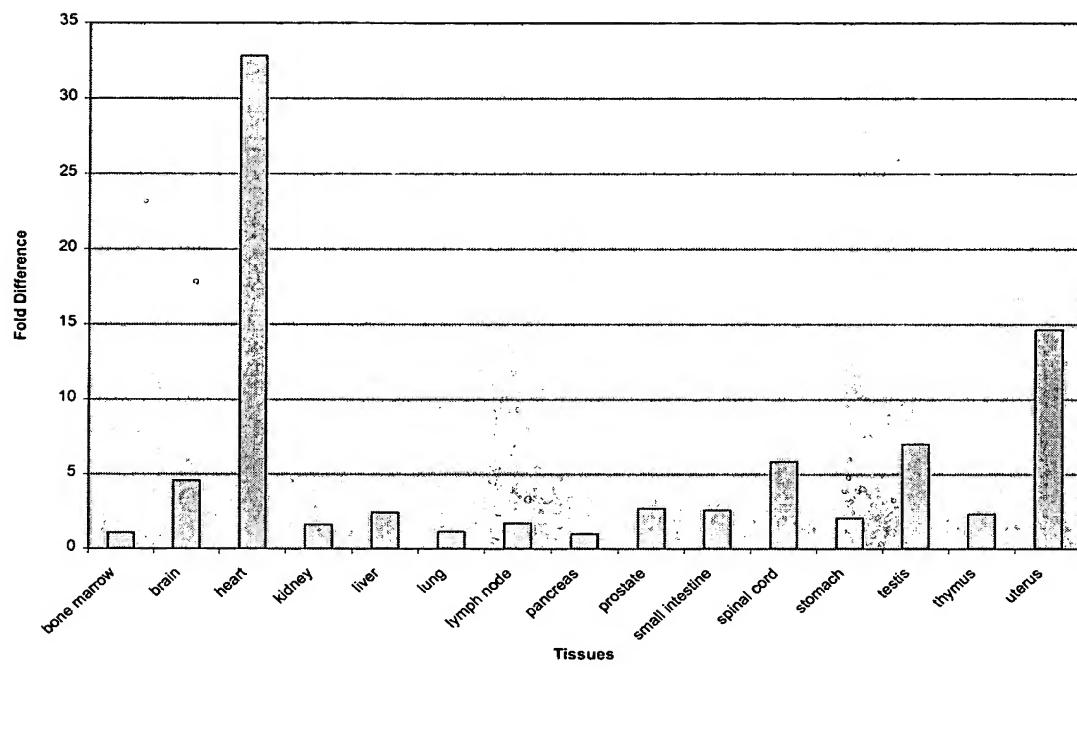


Figure 5

G1934909_001 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA
 cloneE3 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA
 cloneD8 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA

G1934909_001 RIRPNFKGPPVNVTCNIFINSFSSITKTTMACWAPGNGNVSEGPISAPSQDYRVNVFLRQ
 cloneE3 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
 cloneD8 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
 *****:***** : : . . :*****

G1934909_001 QWNDRPLSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV
 cloneE3 QWNDRPLSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV
 cloneD8 QWNDRPLSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV

G1934909_001 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE
 cloneE3 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE
 cloneD8 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE

G1934909_001 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLLERQMGYYLIQMYIPS
 cloneE3 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLLERQMGYYLIQMYIPS
 cloneD8 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLLERQMGYYLIQMYIPS

G1934909_001 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPK-----
 cloneE3 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCL
 cloneD8 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCL

G1934909_001 -----
 cloneE3 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARD
 cloneD8 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARD

G1934909_001 -----
 cloneE3 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD
 cloneD8 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD

Figure 6.

HGRA4

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

HGRA4sv

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

Figure 7

Atgacaactcttgttctgcaaccctctccttccttctggaccctgccagggcaggtcctcctcagggtggcct
tggcaaaagaggaagtcaaatctgaaaccaagggtccagccatgtccccctctgatttccttagacaaaacttatggg
gcgaacatctggatatgtgccaggattcggcccaatttaaggcccacccgtgaacgtgacctgcaacacatcttcatc
aacagtttcagctccatccaagaccacaatggctgtggccctggaatggcaatgtttctgaaggggccatata
ctgcacccctcccaggactaccgggtgaatgtcttcttgccgcaacagtgaaatgaccacgcctgtcctaccgagaata
tcctgatgactcttgacccatcgatccctccatgctgactctatctggaaagccagacctttttgttaatgaaaa
ggggccaacttccatgaggtgaccacggacaacaagttactgcgcacatcttcaagaatggaatgtgtacagcatca
ggctgacccctatttgcctgcctgatggacccatggacatccagacactgcacgatgcagctga
gagcttgcgtacaccatgaaagacctcggtttgagttggctggaaatgtctgttccaaagtggctgaggggctg
actctgcccagtttatctgcggatgagaaggatctaggctgttaccaaagcactacaacacaggaaattcacct
gcatcgaggtaaagttcacctgaaacggcagatggctactatctgattcagatgtacatccccagccactcatcg
catcctgtcctgggtctccttctggatcaacatggatgctgcccctgcccgtggcctggcatcaccaccgtgctc
accatgaccacccagagctggctccggcctttgcctaag (SEQ ID NO:9)

1
2
3
4
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Figure 8

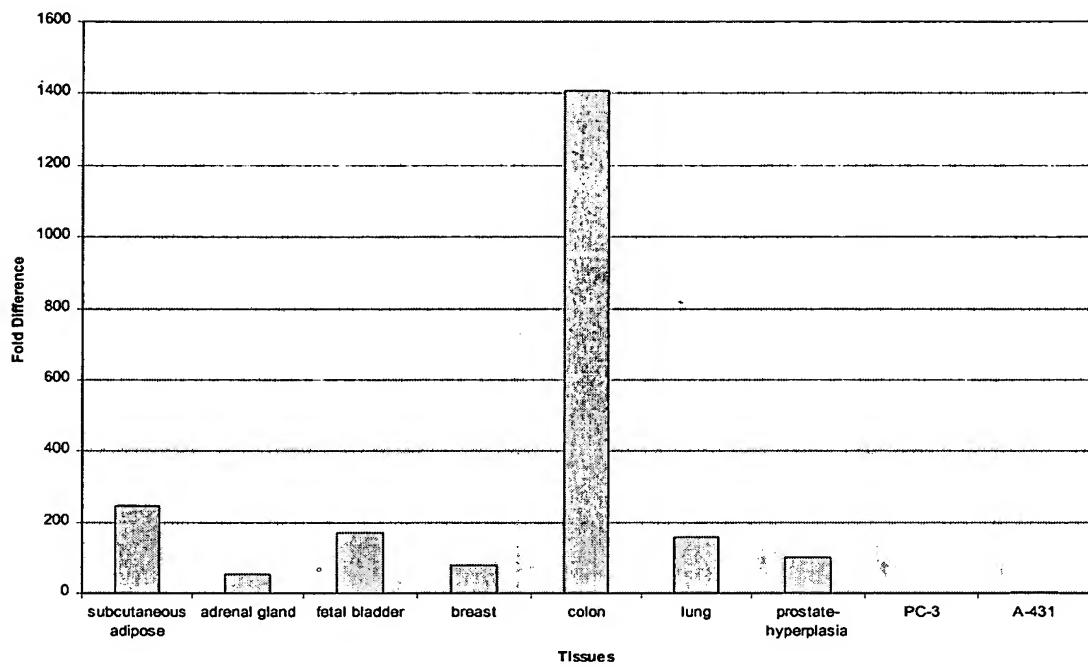


Figure 9

